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1600

RAW SEQUENCE LISTING

DATE: 07/29/2003

PATENT APPLICATION: US/09/319,724B

TIME: 11:33:20

Input Set : A:\aoyama53356 5001us.txt

Output Set: N:\CRF4\07292003\I319724B.raw

3 <110> APPLICANT: VETIGEN
 4 LENZEN, Gerlinde
 5 STROSBURG, Arthur Donny
 6 SUGASAWA, Toshinari
 7 MOROOKA, Shigeaki
 9 <120> TITLE OF INVENTION: MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
 11 <130> FILE REFERENCE: 53356-5001-US
 13 <140> CURRENT APPLICATION NUMBER: US 09/319,724B
 C--> 14 <141> CURRENT FILING DATE: 2003-07-24
 16 <150> PRIOR APPLICATION NUMBER: EP 96402719.7
 17 <151> PRIOR FILING DATE: 1996-12-12
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP97/07339
 20 <151> PRIOR FILING DATE: 1997-12-12
 22 <160> NUMBER OF SEQ ID NOS: 21
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 439
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Homo sapiens
 31 <400> SEQUENCE: 1
 33 Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly Ile Val Gly Glu Ala Asp
 34 1 5 10 15
 37 Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu Glu Ile
 38 20 25 30
 41 Gly Phe Asn Gly Asn Arg Ile Val Asp Val Asn Leu Thr Ser Glu Gly
 42 35 40 45
 45 Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val
 46 50 55 60
 49 Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr
 50 65 70 75 80
 53 Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe
 54 85 90 95
 57 Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile
 58 100 105 110
 61 Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu
 62 115 120 125
 65 Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys
 66 130 135 140
 69 Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe
 70 145 150 155 160
 73 Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile
 74 165 170 175
 77 Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser

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78          180          185          190
81 Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn
82          195          200          205
85 Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp
86          210          215          220
89 Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys
90 225          230          235          240
93 Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser
94          245          250          255
97 Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe
98          260          265          270
101 Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn
102          275          280          285
105 Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg
106          290          295          300
109 Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys
110 305          310          315          320
113 Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe
114          325          330          335
117 Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe
118          340          345          350
121 Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr
122          355          360          365
125 Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln
126          370          375          380
129 Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
130 385          390          395          400
133 Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
134          405          410          415
137 Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu
138          420          425          430
141 Gly Ile Met Cys Gly Ala Ile
142          435
145 <210> SEQ ID NO: 2
146 <211> LENGTH: 1317
147 <212> TYPE: DNA
148 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 2
151 atgtacatag atgatttacc aatatggggt attgttggtg aggctgatga aaatggagaa 60
153 gattactatc tttggacctt taaaaaactt gaaatagggt ttaatggaaa tcgaattgtt 120
155 gatgttaatc taactagtga aggaaagggt aaactgggtc caaatactaa aatccagatg 180
157 tcatattcag taaaatggaa aaagtcagat gtgaaatttg aagatcgatt tgacaaatat 240
159 cttgatccgt ccttttttca acatcggatt cattggtttt caattttcaa ctccttcatg 300
161 atggtgatct tcttggtggg cttagtttca atgattttaa tgagaacatt aagaaaagat 360
163 tatgctcggg acagtaaaga ggaagaaatg gatgatatgg atagagacct aggagatgaa 420
165 tatggatgga aacagggtgca tggagatgta tttagaccat caagtcaccc actgatattt 480
167 tcctctctga ttggttctgg atgtcagata tttgctgtgt ctctcatcgt tattattgtt 540
169 gcaatgatag aagatttata tactgagagg ggatcaatgc tcagtacagc catatttgtc 600
171 tatgctgcta cgtctccagt gaatggttat tttggaggaa gtctgtatgc tagacaagga 660

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173 ggaaggagat ggataaagca gatgtttatt ggggcattcc ttatcccagc tatgggtgtgt 720
175 ggcactgcct tcttcatcaa ttcatagacc atttattacc atgcttcaag agccattcct 780
177 tttggaacaa tgggtggccgt ttgttgcacg tgtttttttg ttattcttcc tctaaatcct 840
179 gttggtacaa tacttggccg aaatctgtca ggtcagccca actttccttg tctgtgcaat 900
181 gctgtgcctc gtcctatacc ggagaaaaaa tggttcatgg agcctgcggt tattgtttgc 960
183 ctgggtggaa ttttaccttt tggttcaatc tttattgaaa tgtatttcat cttcacgtct 1020
185 ttctgggcat ataagatcta ttatgtctat ggcttcatga tgctgggtct ggttatcctg 1080
187 tgcattgtga ctgtctgtgt gactattgtg tgcacatatt ttctactaaa tgcagaagat 1140
189 taccggtggc aatggacaag ttttctctct gctgcatcaa ctgcaatcta tgtttacatg 1200
191 tattcctttt actactattt tttcaaaaaca aagatgtatg gcttatttca aacatcattt 1260
193 tactttggat atatggcggg atttagcaca gccttgggga taatgtgtgg agcgatt 1317

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196 <210> SEQ ID NO: 3

197 <211> LENGTH: 965

198 <212> TYPE: DNA

199 <213> ORGANISM: Homo sapiens

201 <400> SEQUENCE: 3

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202 cagatgtcat attcagtaaa atggaaaaag tcagatgtga aatttgaaga tcgatttgac 60
204 aaatatcttg atccgtcctt ttttcaacat cggattcatt ggttttcaat tttcaactcc 120
206 ttcatgatgg tgatcttctt ggtgggctta gtttcaatga ttttaatgag aacattaaga 180
208 aaagattatg ctcggtacag taaagaggaa gaaatggatg atatggatag agacctagga 240
210 gatgaatatg gatggaaaca ggtgcatgga gatgtattta gaccatcaag tcacccactg 300
212 atattttcct ctctgattgg ttctggatgt cagatatttg ctgtgtctct catcggtatt 360
214 attgttgcaa tgatagaaga tttatatact gagaggggat caatgctcag tacagccata 420
216 tttgtctatg ctgctacgtc tccagtgaat ggttatttta gaggaagtct gtatgctaga 480
218 caaggaggaa ggagatggat aaagcagatg tttattgggg cattccttat cccagctatg 540
220 gtgtgtggca ctgcccttct catcaatttc atagccattt attaccatgc ttcaagagcc 600
222 attccttttg gaacaatggt ggccggttgt tgcattctgt tttttgttat tcttcctcta 660
224 aatcttgttg gtacaatact tggccgaaat ctgtcaggtc agcccaactt tccttgtcgt 720
226 gtcaatgctg tgcctcgtcc tataccggag aaaaaatggt tcatggagcc tgcggttatt 780
228 gtttgccctg gtggaatttt accttttggg tcaatcttta ttgaaatgta tttcatcttc 840
230 acgtctttct gggcatataa gatctattat gtctatggct tcatgatgct ggtgctggtt 900
232 atcctgtgca ttgtgactgt ctgtgtgact attgtgtgca catattttct actaaatgca 960
234 gaaga 965

```

237 <210> SEQ ID NO: 4

238 <211> LENGTH: 285

239 <212> TYPE: DNA

240 <213> ORGANISM: Homo sapiens

242 <400> SEQUENCE: 4

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243 tcagtaaaat gaaaaaagtc agatgtgaaa tttgaagatc gatttgacaa atatcttgat 60
245 ccgtcctttt ttcaacatcg gattcattgg ttttcaattt tcaactcctt catgatgggt 120
247 atcttcttgg tgggcttagt ttcaatgatt ttaatgagaa cattaagaaa agattatgct 180
249 cggtagagta aagaggaaga aatggatgat atggatagag acctaggaga tgaatatgga 240
251 tggaacagg tgcatggaga tgtatttaga ccatcaagtc accca 285

```

254 <210> SEQ ID NO: 5

255 <211> LENGTH: 17

256 <212> TYPE: PRT

257 <213> ORGANISM: Artificial sequence

259 <220> FEATURE:

260 <223> OTHER INFORMATION: Fragment generated by acidic cleavage of polypeptide able to bind ICYP

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262 <400> SEQUENCE: 5
264 Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn
265 1          5          10          15
268 Ser
272 <210> SEQ ID NO: 6
273 <211> LENGTH: 17
274 <212> TYPE: PRT
275 <213> ORGANISM: Artificial sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Fragment generated by acidic cleavage of polypeptide able to
bind ICYP
280 <220> FEATURE:
281 <221> NAME/KEY: MISC_FEATURE
282 <222> LOCATION: (3)..(3)
283 <223> OTHER INFORMATION: Xaa can by any amino acid
286 <400> SEQUENCE: 6
W--> 288 Asp Pro Xaa Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn
289 1          5          10          15
292 His
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 20
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: probe/primer
304 <400> SEQUENCE: 7
305 tcagtaaaat ggaaaaagtc
308 <210> SEQ ID NO: 8
309 <211> LENGTH: 20
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: probe/primer
316 <400> SEQUENCE: 8
317 tgggtgactt gatggtctaa
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 19
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: probe/primer
328 <400> SEQUENCE: 9
329 gctgtgtctc tcatcgтта
332 <210> SEQ ID NO: 10
333 <211> LENGTH: 20
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: probe/primer
340 <400> SEQUENCE: 10

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```

341 ccatccatat tcatctccta                                20
344 <210> SEQ ID NO: 11
345 <211> LENGTH: 21
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: probe/primer
352 <400> SEQUENCE: 11
353 cggtatagga cgaggcacag c                                21
356 <210> SEQ ID NO: 12
357 <211> LENGTH: 18
358 <212> TYPE: DNA
359 <213> ORGANISM: Artificial sequence
361 <220> FEATURE:
362 <223> OTHER INFORMATION: probe/primer
364 <400> SEQUENCE: 12
365 actgaatatg acatctgg                                18
368 <210> SEQ ID NO: 13
369 <211> LENGTH: 1800
370 <212> TYPE: DNA
371 <213> ORGANISM: Homo sapiens
373 <220> FEATURE:
374 <221> NAME/KEY: CDS
375 <222> LOCATION: (3)..(1730)
376 <223> OTHER INFORMATION:
W--> 378 <400> 13
379 cc gcc gcg ctg tgg ctg ctg ctg ctg ctg ccc cgg acc cgg gcg    47
380 Ala Ala Leu Trp Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala
381 1 5 10 15
383 gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc tta tgg    95
384 Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp
385 20 25 30
387 atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat aag tac    143
388 Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr
389 35 40 45
391 ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt cat tac    191
392 Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr
393 50 55 60
395 cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt    239
396 His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser
397 65 70 75
399 ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act tac tgt    287
400 Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys
401 80 85 90 95
403 gaa att gat tta gat aaa gaa aag aga gat gca ttt gta tat gcc ata    335
404 Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile
405 100 105 110
407 aaa aat cat tac tgg tac cag atg tac ata gat gat tta cca ata tgg    383
408 Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/29/2003
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:21

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0

L:378 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:376